

## SEQUENCE LISTING

<110> Commissariat à l'Etude Atomique (CEA)  
Centre National de la Recherche Scientifique (CNRS)

<120> A method for performing restrained dynamics docking of one or  
multiple substrates on multi-specific enzymes

<130> D20647

<150> US 60/421,569

<151> 2002-10-28

<160> 18

<170> PatentIn version 3.2

<210> 1

<211> 403

<212> PRT

<213> Fusarium oxysporum

<220>

<223> P450 Nor, crystal structure from

<400> 1

Met Ala Ser Gly Ala Pro Ser Phe Pro Phe Ser Arg Ala Ser Gly Pro  
1 5 10 15

Glu Pro Pro Ala Glu Phe Ala Lys Leu Arg Ala Thr Asn Pro Val Ser  
20 25 30

Gln Val Lys Leu Phe Asp Gly Ser Leu Ala Trp Leu Val Thr Lys His  
35 40 45

Lys Asp Val Cys Phe Val Ala Thr Ser Glu Lys Leu Ser Lys Val Arg  
50 55 60

Thr Arg Gln Gly Phe Pro Glu Leu Ser Ala Ser Gly Lys Gln Ala Ala  
65 70 75 80

Lys Ala Lys Pro Thr Phe Val Asp Met Asp Pro Pro Glu His Met His  
85 90 95

Gln Arg Ser Met Val Glu Pro Thr Phe Thr Pro Glu Ala Val Lys Asn  
100 105 110

Leu Gln Pro Tyr Ile Gln Arg Thr Val Asp Asp Leu Leu Glu Gln Met  
115 120 125

Lys Gln Lys Gly Cys Ala Asn Gly Pro Val Asp Leu Val Lys Glu Phe  
130 135 140

Ala Leu Pro Val Pro Ser Tyr Ile Ile Tyr Thr Leu Leu Gly Val Pro  
145 150 155 160

Phe Asn Asp Leu Glu Tyr Leu Thr Gln Gln Asn Ala Ile Arg Thr Asn  
165 170 175

Gly Ser Ser Thr Ala Arg Glu Ala Ser Ala Ala Asn Gln Glu Leu Leu  
 180 185 190  
 Asp Tyr Leu Ala Ile Leu Val Glu Gln Arg Leu Val Glu Pro Lys Asp  
 195 200 205  
 Asp Ile Ile Ser Lys Leu Cys Thr Glu Gln Val Lys Pro Gly Asn Ile  
 210 215 220  
 Asp Lys Ser Asp Ala Val Gln Ile Ala Phe Leu Leu Leu Val Ala Gly  
 225 230 235 240  
 Asn Ala Thr Met Val Asn Met Ile Ala Leu Gly Val Ala Thr Leu Ala  
 245 250 255  
 Gln His Pro Asp Gln Leu Ala Gln Leu Lys Ala Asn Pro Ser Leu Ala  
 260 265 270  
 Pro Gln Phe Val Glu Glu Leu Cys Arg Tyr His Thr Ala Ser Ala Leu  
 275 280 285  
 Ala Ile Lys Arg Thr Ala Lys Glu Asp Val Met Ile Gly Asp Lys Leu  
 290 295 300  
 Val Arg Ala Asn Glu Gly Ile Ile Ala Ser Asn Gln Ser Ala Asn Arg  
 305 310 315 320  
 Asp Glu Glu Val Phe Glu Asn Pro Asp Glu Phe Asn Met Asn Arg Lys  
 325 330 335  
 Trp Pro Pro Gln Asp Pro Leu Gly Phe Gly Phe Gly Asp His Arg Cys  
 340 345 350  
 Ile Ala Glu His Leu Ala Lys Ala Glu Leu Thr Thr Val Phe Ser Thr  
 355 360 365  
 Leu Tyr Gln Lys Phe Pro Asp Leu Lys Val Ala Val Pro Leu Gly Lys  
 370 375 380  
 Ile Asn Tyr Thr Pro Leu Asn Arg Asp Val Gly Ile Val Asp Leu Pro  
 385 390 395 400  
 Val Ile Phe

&lt;210&gt; 2

&lt;211&gt; 403

&lt;212&gt; PRT

&lt;213&gt; Saccharopolyspora erythraea

&lt;220&gt;

&lt;223&gt; P450 EryF, crystal structure loxa

&lt;400&gt; 2

Ala Thr Val Pro Asp Leu Glu Ser Asp Ser Phe His Val Asp Trp Tyr  
 1 5 10 15  
 Ser Thr Tyr Ala Glu Leu Arg Glu Thr Ala Pro Val Thr Pro Val Arg  
 20 25 30

Phe Leu Gly Gln Asp Ala Trp Leu Val Thr Gly Tyr Asp Glu Ala Lys  
 35 40 45  
 Ala Ala Leu Ser Asp Leu Arg Leu Ser Ser Asp Pro Lys Lys Lys Tyr  
 50 55 60  
 Pro Gly Val Glu Val Glu Phe Pro Ala Tyr Leu Gly Phe Pro Glu Asp  
 65 70 75 80  
 Val Arg Asn Tyr Phe Ala Thr Asn Met Gly Thr Ser Asp Pro Pro Thr  
 85 90 95  
 His Thr Arg Leu Arg Lys Leu Val Ser Gln Glu Phe Thr Val Arg Arg  
 100 105 110  
 Val Glu Ala Met Arg Pro Arg Val Glu Gln Ile Thr Ala Glu Leu Leu  
 115 120 125  
 Asp Glu Val Gly Asp Ser Gly Val Val Asp Ile Val Asp Arg Phe Ala  
 130 135 140  
 His Pro Leu Pro Ile Lys Val Ile Cys Glu Leu Leu Gly Val Asp Glu  
 145 150 155 160  
 Ala Ala Arg Gly Ala Phe Gly Arg Trp Ser Ser Glu Ile Leu Val Met  
 165 170 175  
 Asp Pro Glu Arg Ala Glu Gln Arg Gly Gln Ala Ala Arg Glu Val Val  
 180 185 190  
 Asn Phe Ile Leu Asp Leu Val Glu Arg Arg Arg Thr Glu Pro Gly Asp  
 195 200 205  
 Asp Leu Leu Ser Ala Leu Ile Ser Val Gln Asp Asp Asp Asp Gly Arg  
 210 215 220  
 Leu Ser Ala Asp Glu Leu Thr Ser Ile Ala Leu Val Leu Leu Leu Ala  
 225 230 235 240  
 Gly Phe Glu Ala Ser Val Ser Leu Ile Gly Ile Gly Thr Tyr Leu Leu  
 245 250 255  
 Leu Thr His Pro Asp Gln Leu Ala Leu Val Arg Ala Asp Pro Ser Ala  
 260 265 270  
 Leu Pro Asn Ala Val Glu Glu Ile Leu Arg Tyr Ile Ala Pro Pro Glu  
 275 280 285  
 Thr Thr Thr Arg Phe Ala Ala Glu Glu Val Glu Ile Gly Gly Val Ala  
 290 295 300  
 Ile Pro Gln Tyr Ser Thr Val Leu Val Ala Asn Gly Ala Ala Asn Arg  
 305 310 315 320  
 Asp Pro Ser Gln Phe Pro Asp Pro His Arg Phe Asp Val Thr Arg Asp  
 325 330 335  
 Thr Arg Gly His Leu Ser Phe Gly Gln Gly Ile His Phe Cys Met Gly  
 340 345 350  
 Arg Pro Leu Ala Lys Leu Glu Gly Glu Val Ala Leu Arg Ala Leu Phe

355                      360                      365  
 Gly Arg Phe Pro Ala Leu Ser Leu Gly Ile Asp Ala Asp Asp Val Val  
     370                      375                      380  
 Trp Arg Arg Ser Leu Leu Leu Arg Gly Ile Asp His Leu Pro Val Arg  
     385                      390                      395                      400  
 Leu Asp Gly

<210> 3  
 <211> 412  
 <212> PRT  
 <213> Pseudomonas sp.

<220>  
 <223> P450 Terp, crystal structure 1cpt

<400> 3

Met Asp Ala Arg Ala Thr Ile Pro Glu His Ile Ala Arg Thr Val Ile  
     1                      5                      10                      15  
 Leu Pro Gln Gly Tyr Ala Asp Asp Glu Val Ile Tyr Pro Ala Phe Lys  
                     20                      25                      30  
 Trp Leu Arg Asp Glu Gln Pro Leu Ala Met Ala His Ile Glu Gly Tyr  
                     35                      40                      45  
 Asp Pro Met Trp Ile Ala Thr Lys His Ala Asp Val Met Gln Ile Gly  
                     50                      55                      60  
 Lys Gln Pro Gly Leu Phe Ser Asn Ala Glu Gly Ser Glu Ile Leu Tyr  
     65                      70                      75                      80  
 Asp Gln Asn Asn Glu Ala Phe Met Arg Ser Ile Ser Gly Gly Cys Pro  
                     85                      90                      95  
 His Val Ile Asp Ser Leu Thr Ser Met Asp Pro Pro Thr His Thr Ala  
                     100                      105                      110  
 Tyr Arg Gly Leu Thr Leu Asn Trp Phe Gln Pro Ala Ser Ile Arg Lys  
                     115                      120                      125  
 Leu Glu Glu Asn Ile Arg Arg Ile Ala Gln Ala Ser Val Gln Arg Leu  
                     130                      135                      140  
 Leu Asp Phe Asp Gly Glu Cys Asp Phe Met Thr Asp Cys Ala Leu Tyr  
     145                      150                      155                      160  
 Tyr Pro Leu His Val Val Met Thr Ala Leu Gly Val Pro Glu Asp Asp  
                     165                      170                      175  
 Glu Pro Leu Met Leu Lys Leu Thr Gln Asp Phe Phe Gly Val Glu Ala  
                     180                      185                      190  
 Ala Arg Arg Phe His Glu Thr Ile Ala Thr Phe Tyr Asp Tyr Phe Asn  
                     195                      200                      205  
 Gly Phe Thr Val Asp Arg Arg Ser Cys Pro Lys Asp Asp Val Met Ser

5/31

210                      215                      220  
 Leu Leu Ala Asn Ser Lys Leu Asp Gly Asn Tyr Ile Asp Asp Lys Tyr  
 225                      230                      235                      240  
 Ile Asn Ala Tyr Tyr Val Ala Ile Ala Thr Ala Gly His Asp Thr Thr  
                     245                      250                      255  
 Ser Ser Ser Ser Gly Gly Ala Ile Ile Gly Leu Ser Arg Asn Pro Glu  
                     260                      265                      270  
 Gln Leu Ala Leu Ala Lys Ser Asp Pro Ala Leu Ile Pro Arg Leu Val  
                     275                      280                      285  
 Asp Glu Ala Val Arg Trp Thr Ala Pro Val Lys Ser Phe Met Arg Thr  
                     290                      295                      300  
 Ala Leu Ala Asp Thr Glu Val Arg Gly Gln Asn Ile Lys Arg Gly Asp  
 305                      310                      315                      320  
 Arg Ile Met Leu Ser Tyr Pro Ser Ala Asn Arg Asp Glu Glu Val Phe  
                     325                      330                      335  
 Ser Asn Pro Asp Glu Phe Asp Ile Thr Arg Phe Pro Asn Arg His Leu  
                     340                      345                      350  
 Gly Phe Gly Trp Gly Ala His Met Cys Leu Gly Gln His Leu Ala Lys  
                     355                      360                      365  
 Leu Glu Met Lys Ile Phe Phe Glu Glu Leu Leu Pro Lys Leu Lys Ser  
                     370                      375                      380  
 Val Glu Leu Ser Gly Pro Pro Arg Leu Val Ala Thr Asn Phe Val Gly  
 385                      390                      395                      400  
 Gly Pro Lys Asn Val Pro Ile Arg Phe Thr Lys Ala  
                     405                      410

&lt;210&gt; 4

&lt;211&gt; 414

&lt;212&gt; PRT

&lt;213&gt; Pseudomonas putida

&lt;220&gt;

&lt;223&gt; P450 Cam, crystal structure 3cpp

&lt;400&gt; 4

Thr Thr Glu Thr Ile Gln Ser Asn Ala Asn Leu Ala Pro Leu Pro Pro  
 1                      5                      10                      15  
 His Val Pro Glu His Leu Val Phe Asp Phe Asp Met Tyr Asn Pro Ser  
                     20                      25                      30  
 Asn Leu Ser Ala Gly Val Gln Glu Ala Trp Ala Val Leu Gln Glu Ser  
                     35                      40                      45  
 Asn Val Pro Asp Leu Val Trp Thr Arg Cys Asn Gly Gly His Trp Ile  
                     50                      55                      60  
 Ala Thr Arg Gly Gln Leu Ile Arg Glu Ala Tyr Glu Asp Tyr Arg His

6/31

65	70					75					80				
Phe Ser Ser Glu Cys Pro Phe Ile Pro Arg Glu Ala Gly Glu Ala Tyr	85					90					95				
Asp Phe Ile Pro Thr Ser Met Asp Pro Pro Glu Gln Arg Gln Phe Arg	100					105					110				
Ala Leu Ala Asn Gln Val Val Gly Met Pro Val Val Asp Lys Leu Glu	115					120					125				
Asn Arg Ile Gln Glu Leu Ala Cys Ser Leu Ile Glu Ser Leu Arg Pro	130					135					140				
Gln Gly Gln Cys Asn Phe Thr Glu Asp Tyr Ala Glu Pro Phe Pro Ile	145					150					155				
Arg Ile Phe Met Leu Leu Ala Gly Leu Pro Glu Glu Asp Ile Pro His	165					170					175				
Leu Lys Tyr Leu Thr Asp Gln Met Thr Arg Pro Asp Gly Ser Met Thr	180					185					190				
Phe Ala Glu Ala Lys Glu Ala Leu Tyr Asp Tyr Leu Ile Pro Ile Ile	195					200					205				
Glu Gln Arg Arg Gln Lys Pro Gly Thr Asp Ala Ile Ser Ile Val Ala	210					215					220				
Asn Gly Gln Val Asn Gly Arg Pro Ile Thr Ser Asp Glu Ala Lys Arg	225					230					235				
Met Cys Gly Leu Leu Leu Val Gly Gly Leu Asp Thr Val Val Asn Phe	245					250					255				
Leu Ser Phe Ser Met Glu Phe Leu Ala Lys Ser Pro Glu His Arg Gln	260					265					270				
Glu Leu Ile Glu Arg Pro Glu Arg Ile Pro Ala Ala Cys Glu Glu Leu	275					280					285				
Leu Arg Arg Phe Ser Leu Val Ala Asp Gly Arg Ile Leu Thr Ser Asp	290					295					300				
Tyr Glu Phe His Gly Val Gln Leu Lys Lys Gly Asp Gln Ile Leu Leu	305					310					315				
Pro Gln Met Leu Ser Gly Leu Asp Glu Arg Glu Asn Ala Cys Pro Met	325					330					335				
His Val Asp Phe Ser Arg Gln Lys Val Ser His Thr Thr Phe Gly His	340					345					350				
Gly Ser His Leu Cys Leu Gly Gln His Leu Ala Arg Arg Glu Ile Ile	355					360					365				
Val Thr Leu Lys Glu Trp Leu Thr Arg Ile Pro Asp Phe Ser Ile Ala	370					375					380				
Pro Gly Ala Gln Ile Gln His Lys Ser Gly Ile Val Ser Gly Val Gln	385					390					395				
											400				

Ala Leu Pro Leu Val Trp Asp Pro Ala Thr Thr Lys Ala Val  
 405 410

<210> 5

<211> 471

<212> PRT

<213> Bacillus megaterium

<220>

<223> P450 BM3, crystal structure 2hpd

<400> 5

Thr Ile Lys Glu Met Pro Gln Pro Lys Thr Phe Gly Glu Leu Lys Asn  
 1 5 10 15

Leu Pro Leu Leu Asn Thr Asp Lys Pro Val Gln Ala Leu Met Lys Ile  
 20 25 30

Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg Val  
 35 40 45

Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp Glu  
 50 55 60

Ser Arg Phe Asp Lys Asn Leu Ser Gln Ala Leu Lys Phe Val Arg Asp  
 65 70 75 80

Phe Ala Gly Asp Gly Leu Phe Thr Ser Trp Thr His Glu Lys Asn Trp  
 85 90 95

Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala Met  
 100 105 110

Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val Gln  
 115 120 125

Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu Asp  
 130 135 140

Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn Tyr  
 145 150 155 160

Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr Ser  
 165 170 175

Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala Asn  
 180 185 190

Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu Asp  
 195 200 205

Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg Lys  
 210 215 220

Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn Gly  
 225 230 235 240

Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg Tyr

	245		250		255
Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly Leu	260		265		270
Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu Gln	275		280		285
Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Val Pro Ser	290		295		300
Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn Glu	305		310		315
Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala Lys	325		330		335
Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp Glu	340		345		350
Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp Gly	355		360		365
Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser Ala	370		375		380
Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala Cys	385		390		395
Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly Met	405		410		415
Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu Asp	420		425		430
Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys Ala	435		440		445
Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr Glu	450		455		460
Gln Ser Ala Lys Lys Val Arg	465		470		

&lt;210&gt; 6

&lt;211&gt; 473

&lt;212&gt; PRT

&lt;213&gt; Rabbit

&lt;220&gt;

&lt;223&gt; P450 2C5, crystal structure 1dt6

&lt;400&gt; 6

Met Ala Lys Lys Thr Ser Ser Lys Gly Lys Leu Pro Pro Gly Pro Thr	1	5	10	15
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Pro Phe Pro Ile Ile Gly Asn Ile Leu Gln Ile Asp Ala Lys Asp Ile	20	25	30
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Ser Lys Ser Leu Thr Lys Phe Ser Glu Cys Tyr Gly Pro Val Phe Thr  
 35 40 45  
 Val Tyr Leu Gly Met Lys Pro Thr Val Val Leu His Gly Tyr Glu Ala  
 50 55 60  
 Val Lys Glu Ala Leu Val Asp Leu Gly Glu Glu Phe Ala Gly Arg Gly  
 65 70 75 80  
 Ser Val Pro Ile Leu Glu Lys Val Ser Lys Gly Leu Gly Ile Ala Phe  
 85 90 95  
 Ser Asn Ala Lys Thr Trp Lys Glu Met Arg Arg Phe Ser Leu Met Thr  
 100 105 110  
 Leu Arg Asn Phe Gly Met Gly Lys Arg Ser Ile Glu Asp Arg Ile Gln  
 115 120 125  
 Glu Glu Ala Arg Cys Leu Val Glu Glu Leu Arg Lys Thr Asn Ala Ser  
 130 135 140  
 Pro Cys Asp Pro Thr Phe Ile Leu Gly Cys Ala Pro Cys Asn Val Ile  
 145 150 155 160  
 Cys Ser Val Ile Phe His Asn Arg Phe Asp Tyr Lys Asp Glu Glu Phe  
 165 170 175  
 Leu Lys Leu Met Glu Ser Leu His Glu Asn Val Glu Leu Leu Gly Thr  
 180 185 190  
 Pro Trp Leu Gln Val Tyr Asn Asn Phe Pro Ala Leu Leu Asp Tyr Phe  
 195 200 205  
 Pro Gly Ile His Lys Thr Leu Leu Lys Asn Ala Asp Tyr Ile Lys Asn  
 210 215 220  
 Phe Ile Met Glu Lys Val Lys Glu His Gln Lys Leu Leu Asp Val Asn  
 225 230 235 240  
 Asn Pro Arg Asp Phe Ile Asp Cys Phe Leu Ile Lys Met Glu Gln Glu  
 245 250 255  
 Asn Asn Leu Glu Phe Thr Leu Glu Ser Leu Val Ile Ala Val Ser Asp  
 260 265 270  
 Leu Phe Gly Ala Gly Thr Glu Thr Thr Ser Thr Thr Leu Arg Tyr Ser  
 275 280 285  
 Leu Leu Leu Leu Lys His Pro Glu Val Ala Ala Arg Val Gln Glu  
 290 295 300  
 Glu Ile Glu Arg Val Ile Gly Arg His Arg Ser Pro Cys Met Gln Asp  
 305 310 315 320  
 Arg Ser Arg Met Pro Tyr Thr Asp Ala Val Ile His Glu Ile Gln Arg  
 325 330 335  
 Phe Ile Asp Leu Leu Pro Thr Asn Leu Pro His Ala Val Thr Arg Asp  
 340 345 350  
 Val Arg Phe Arg Asn Tyr Phe Ile Pro Lys Gly Thr Asp Ile Ile Thr

10/31

355                      360                      365  
 Ser Leu Thr Ser Val Leu His Asp Glu Lys Ala Phe Pro Asn Pro Lys  
     370                      375                      380  
 Val Phe Asp Pro Gly His Phe Leu Asp Glu Ser Gly Asn Phe Lys Lys  
     385                      390                      395                      400  
 Ser Asp Tyr Phe Met Pro Phe Ser Ala Gly Lys Arg Met Cys Val Gly  
                     405                      410                      415  
 Glu Gly Leu Ala Arg Met Glu Leu Phe Leu Phe Leu Thr Ser Ile Leu  
                     420                      425                      430  
 Gln Asn Phe Lys Leu Gln Ser Leu Val Glu Pro Lys Asp Leu Asp Ile  
                     435                      440                      445  
 Thr Ala Val Val Asn Gly Phe Val Ser Val Pro Pro Ser Tyr Gln Leu  
     450                      455                      460  
 Cys Phe Ile Pro Ile His His His His  
     465                      470  
  
 <210> 7  
 <211> 487  
 <212> PRT  
 <213> Rabbit  
  
 <220>  
 <223> P450 2C5  
  
 <400> 7  
  
 Met Asp Pro Val Val Val Leu Val Leu Gly Leu Cys Cys Leu Leu Leu  
     1                      5                      10                      15  
 Leu Ser Ile Trp Lys Gln Asn Ser Gly Arg Gly Lys Leu Pro Pro Gly  
                     20                      25                      30  
 Pro Thr Pro Phe Pro Ile Ile Gly Asn Ile Leu Gln Ile Asp Ala Lys  
                     35                      40                      45  
 Asp Ile Ser Lys Ser Leu Thr Lys Phe Ser Glu Cys Tyr Gly Pro Val  
     50                      55                      60  
 Phe Thr Val Tyr Leu Gly Met Lys Pro Thr Val Val Leu His Gly Tyr  
     65                      70                      75                      80  
 Glu Ala Val Lys Glu Ala Leu Val Asp Leu Gly Glu Glu Phe Ala Gly  
                     85                      90                      95  
 Thr Gly Ser Val Pro Ile Leu Glu Lys Val Ser Lys Gly Leu Gly Ile  
                     100                      105                      110  
 Ala Phe Ser Asn Ala Lys Thr Trp Lys Glu Met Arg Arg Phe Ser Leu  
     115                      120                      125  
 Met Thr Leu Arg Asn Phe Gly Met Gly Lys Arg Ser Ile Glu Asp Arg  
     130                      135                      140

11/31

Ile	Gln	Glu	Glu	Ala	Arg	Cys	Leu	Val	Glu	Glu	Leu	Arg	Lys	Thr	Asn	145	150	155	160
Ala	Ser	Pro	Cys	Asp	Pro	Thr	Phe	Ile	Leu	Gly	Cys	Ala	Pro	Cys	Asn	165	170	175	
Val	Ile	Cys	Ser	Val	Ile	Phe	His	Asn	Arg	Phe	Asp	Tyr	Lys	Asp	Glu	180	185	190	
Glu	Phe	Leu	Lys	Leu	Met	Glu	Ser	Leu	Asn	Glu	Asn	Val	Arg	Ile	Leu	195	200	205	
Ser	Ser	Pro	Trp	Leu	Gln	Val	Tyr	Asn	Asn	Phe	Pro	Ala	Leu	Leu	Asp	210	215	220	
Tyr	Phe	Pro	Gly	Ile	His	Lys	Thr	Leu	Leu	Lys	Asn	Ala	Asp	Tyr	Ile	225	230	235	240
Lys	Asn	Phe	Ile	Met	Glu	Lys	Val	Lys	Glu	His	Glu	Lys	Leu	Leu	Asp	245	250	255	
Val	Asn	Asn	Pro	Arg	Asp	Phe	Ile	Asp	Cys	Phe	Leu	Ile	Lys	Met	Glu	260	265	270	
Gln	Glu	Asn	Asn	Leu	Glu	Phe	Thr	Leu	Glu	Ser	Leu	Val	Ile	Ala	Val	275	280	285	
Ser	Asp	Leu	Phe	Gly	Ala	Gly	Thr	Glu	Thr	Thr	Ser	Thr	Thr	Leu	Arg	290	295	300	
Tyr	Ser	Leu	Leu	Leu	Leu	Leu	Lys	His	Pro	Glu	Val	Ala	Ala	Arg	Val	305	310	315	320
Gln	Glu	Glu	Ile	Glu	Arg	Val	Ile	Gly	Arg	His	Arg	Ser	Pro	Cys	Met	325	330	335	
Gln	Asp	Arg	Ser	Arg	Met	Pro	Tyr	Thr	Asp	Ala	Val	Ile	His	Glu	Ile	340	345	350	
Gln	Arg	Phe	Ile	Asp	Leu	Leu	Pro	Thr	Asn	Leu	Pro	His	Ala	Val	Thr	355	360	365	
Arg	Asp	Val	Arg	Phe	Arg	Asn	Tyr	Phe	Ile	Pro	Lys	Gly	Thr	Asp	Ile	370	375	380	
Ile	Thr	Ser	Leu	Thr	Ser	Val	Leu	His	Asp	Glu	Lys	Ala	Phe	Pro	Asn	385	390	395	400
Pro	Lys	Val	Phe	Asp	Pro	Gly	His	Phe	Leu	Asp	Glu	Ser	Gly	Asn	Phe	405	410	415	
Lys	Lys	Ser	Asp	Tyr	Phe	Met	Pro	Phe	Ser	Ala	Gly	Lys	Arg	Met	Cys	420	425	430	
Val	Gly	Glu	Gly	Leu	Ala	Arg	Met	Glu	Leu	Phe	Leu	Phe	Leu	Thr	Ser	435	440	445	
Ile	Leu	Gln	Asn	Phe	Lys	Leu	Gln	Ser	Leu	Val	Glu	Pro	Lys	Asp	Leu	450	455	460	
Asp	Ile	Thr	Ala	Val	Val	Asn	Gly	Phe	Val	Ser	Val	Pro	Pro	Ser	Tyr				

465 470 475 480

Gln Leu Cys Phe Ile Pro Ile  
485

<210> 8  
<211> 455  
<212> PRT  
<213> Mycobacterium tuberculosis

<220>  
<223> CYP51, crystal structure 1e9x

<400> 8

Met Ser Ala Val Ala Leu Pro Arg Val Ser Gly Gly His Asp Glu His  
1 5 10 15

Gly His Leu Glu Glu Phe Arg Thr Asp Pro Ile Gly Leu Met Gln Arg  
20 25 30

Val Arg Asp Glu Cys Gly Asp Val Gly Thr Phe Gln Leu Ala Gly Lys  
35 40 45

Gln Val Val Leu Leu Ser Gly Ser His Ala Asn Glu Phe Phe Phe Arg  
50 55 60

Ala Gly Asp Asp Asp Leu Asp Gln Ala Lys Ala Tyr Pro Phe Met Thr  
65 70 75 80

Pro Ile Phe Gly Glu Gly Val Val Phe Asp Ala Ser Pro Glu Arg Arg  
85 90 95

Lys Glu Met Leu His Asn Ala Ala Leu Arg Gly Glu Gln Met Lys Gly  
100 105 110

His Ala Ala Thr Ile Glu Asp Gln Val Arg Arg Met Ile Ala Asp Trp  
115 120 125

Gly Glu Ala Gly Glu Ile Asp Leu Leu Asp Phe Phe Ala Glu Leu Thr  
130 135 140

Ile Tyr Thr Ser Ser Ala Cys Leu Ile Gly Lys Lys Phe Arg Asp Gln  
145 150 155 160

Leu Asp Gly Arg Phe Ala Lys Leu Tyr His Glu Leu Glu Arg Gly Thr  
165 170 175

Asp Pro Leu Ala Tyr Val Asp Pro Tyr Leu Pro Ile Glu Ser Phe Arg  
180 185 190

Arg Arg Asp Glu Ala Arg Asn Gly Leu Val Ala Leu Val Ala Asp Ile  
195 200 205

Met Asn Gly Arg Ile Ala Asn Pro Pro Thr Asp Lys Ser Asp Arg Asp  
210 215 220

Met Leu Asp Val Leu Ile Ala Val Lys Ala Glu Thr Gly Thr Pro Arg  
225 230 235 240

Phe Ser Ala Asp Glu Ile Thr Gly Met Phe Ile Ser Met Met Phe Ala  
 245 250 255  
 Gly His His Thr Ser Ser Gly Thr Ala Ser Trp Thr Leu Ile Glu Leu  
 260 265 270  
 Met Arg His Arg Asp Ala Tyr Ala Ala Val Ile Asp Glu Leu Asp Glu  
 275 280 285  
 Leu Tyr Gly Asp Gly Arg Ser Val Ser Phe His Ala Leu Arg Gln Ile  
 290 295 300  
 Pro Gln Leu Glu Asn Val Leu Lys Glu Thr Leu Arg Leu His Pro Pro  
 305 310 315 320  
 Leu Ile Ile Leu Met Arg Val Ala Lys Gly Glu Phe Glu Val Gln Gly  
 325 330 335  
 His Arg Ile His Glu Gly Asp Leu Val Ala Ala Ser Pro Ala Ile Ser  
 340 345 350  
 Asn Arg Ile Pro Glu Asp Phe Pro Asp Pro His Asp Phe Val Pro Ala  
 355 360 365  
 Arg Tyr Glu Gln Pro Arg Gln Glu Asp Leu Leu Asn Arg Trp Thr Trp  
 370 375 380  
 Ile Pro Phe Gly Ala Gly Arg His Arg Cys Val Gly Ala Ala Phe Ala  
 385 390 395 400  
 Ile Met Gln Ile Lys Ala Ile Phe Ser Val Leu Leu Arg Glu Tyr Glu  
 405 410 415  
 Phe Glu Met Ala Gln Pro Pro Glu Ser Tyr Arg Asn Asp His Ser Lys  
 420 425 430  
 Met Val Val Gln Leu Ala Gln Pro Ala Cys Val Arg Tyr Arg Arg Arg  
 435 440 445  
 Thr Gly Val His His His His  
 450 455

<210> 9  
 <211> 504  
 <212> PRT  
 <213> Rat

<220>  
 <223> CYP3A1

<400> 9

Met Asp Leu Leu Ser Ala Leu Thr Leu Glu Thr Trp Val Leu Leu Ala  
 1 5 10 15  
 Val Val Leu Val Leu Leu Tyr Gly Phe Gly Thr Arg Thr His Gly Leu  
 20 25 30  
 Phe Lys Lys Gln Gly Ile Pro Gly Pro Lys Pro Leu Pro Phe Phe Gly  
 35 40 45

Thr Val Leu Asn Tyr Tyr Met Gly Leu Trp Lys Phe Asp Val Glu Cys  
 50 55 60  
 His Lys Lys Tyr Gly Lys Ile Trp Gly Leu Phe Asp Gly Gln Met Pro  
 65 70 75 80  
 Leu Phe Ala Ile Thr Asp Thr Glu Met Ile Lys Asn Val Leu Val Lys  
 85 90 95  
 Glu Cys Phe Ser Val Phe Thr Asn Arg Arg Asp Phe Gly Pro Val Gly  
 100 105 110  
 Ile Met Gly Lys Ala Val Ser Val Ala Lys Asp Glu Glu Trp Lys Arg  
 115 120 125  
 Tyr Arg Ala Leu Leu Ser Pro Thr Phe Thr Ser Gly Arg Leu Lys Glu  
 130 135 140  
 Met Phe Pro Ile Ile Glu Gln Tyr Gly Asp Ile Leu Val Lys Tyr Leu  
 145 150 155 160  
 Lys Gln Glu Ala Glu Thr Gly Lys Pro Val Thr Met Lys Lys Val Phe  
 165 170 175  
 Gly Ala Tyr Ser Met Asp Val Ile Thr Ser Thr Ser Phe Gly Val Asn  
 180 185 190  
 Val Asp Ser Leu Asn Asn Pro Lys Asp Pro Phe Val Glu Lys Thr Lys  
 195 200 205  
 Lys Leu Leu Arg Phe Asp Phe Phe Asp Pro Leu Phe Leu Ser Val Val  
 210 215 220  
 Leu Phe Pro Phe Leu Thr Pro Ile Tyr Glu Met Leu Asn Ile Cys Met  
 225 230 235 240  
 Phe Pro Lys Asp Ser Ile Glu Phe Phe Lys Lys Phe Val Tyr Arg Met  
 245 250 255  
 Lys Glu Thr Arg Leu Asp Ser Val Gln Lys His Arg Val Asp Phe Leu  
 260 265 270  
 Gln Leu Met Met Asn Ala His Asn Asp Ser Lys Asp Lys Glu Ser His  
 275 280 285  
 Thr Ala Leu Ser Asp Met Glu Ile Thr Ala Gln Ser Ile Ile Phe Ile  
 290 295 300  
 Phe Ala Gly Tyr Glu Pro Thr Ser Ser Thr Leu Ser Phe Val Leu His  
 305 310 315 320  
 Ser Leu Ala Thr His Pro Asp Thr Gln Lys Lys Leu Gln Glu Glu Ile  
 325 330 335  
 Asp Arg Ala Leu Pro Asn Lys Ala Pro Pro Thr Tyr Asp Thr Val Met  
 340 345 350  
 Glu Met Glu Tyr Leu Asp Met Val Leu Asn Glu Thr Leu Arg Leu Tyr  
 355 360 365

Pro Ile Gly Asn Arg Leu Glu Arg Val Cys Lys Lys Asp Val Glu Ile  
 370 375 380  
 Asn Gly Val Phe Met Pro Lys Gly Ser Val Val Met Ile Pro Ser Tyr  
 385 390 395 400  
 Ala Leu His Arg Asp Pro Gln His Trp Pro Glu Pro Glu Glu Phe Arg  
 405 410 415  
 Pro Glu Arg Phe Ser Lys Glu Asn Lys Gly Ser Ile Asp Pro Tyr Val  
 420 425 430  
 Tyr Leu Pro Phe Gly Asn Gly Pro Arg Asn Cys Ile Gly Met Arg Phe  
 435 440 445  
 Ala Leu Met Asn Met Lys Leu Ala Leu Thr Lys Val Leu Gln Asn Phe  
 450 455 460  
 Ser Phe Gln Pro Cys Lys Glu Thr Gln Ile Pro Leu Lys Leu Ser Arg  
 465 470 475 480  
 Gln Gly Leu Leu Gln Pro Thr Lys Pro Ile Ile Leu Lys Val Val Pro  
 485 490 495  
 Arg Asp Glu Ile Ile Thr Gly Ser  
 500

<210> 10  
 <211> 503  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> CYP3A3

<400> 10

Ala Leu Ile Pro Asp Leu Ala Met Glu Thr Trp Leu Leu Leu Ala Val  
 1 5 10 15  
 Ser Leu Val Leu Leu Tyr Leu Tyr Gly Thr His Ser His Gly Leu Phe  
 20 25 30  
 Lys Lys Leu Gly Ile Pro Gly Pro Thr Pro Leu Pro Phe Leu Gly Asn  
 35 40 45  
 Ile Leu Ser Tyr His Lys Gly Phe Cys Met Phe Asp Met Glu Cys His  
 50 55 60  
 Lys Lys Tyr Gly Lys Val Trp Gly Phe Tyr Asp Gly Gln Gln Pro Val  
 65 70 75 80  
 Leu Ala Ile Thr Asp Pro Asp Met Ile Lys Leu Val Leu Val Lys Glu  
 85 90 95  
 Cys Tyr Ser Val Phe Thr Asn Arg Glu Pro Phe Gly Pro Val Gly Phe  
 100 105 110  
 Met Lys Ser Ala Ile Ser Ile Ala Glu Asp Glu Glu Trp Lys Arg Leu

115	120	125
Arg Ser Leu Leu Ser Pro Thr Phe Thr Ser Gly Lys Leu Lys Glu Met 130 135 140		
Val Pro Ile Ile Ala Gln Tyr Gly Asp Val Leu Val Arg Asn Leu Arg 145 150 155 160		
Arg Glu Arg Glu Thr Gly Lys Pro Val Thr Leu Lys Asp Val Phe Gly 165 170 175		
Ala Tyr Ser Met Asp Val Ile Thr Ser Ser Ser Phe Gly Val Asn Val 180 185 190		
Asp Ser Leu Asn Asn Pro Gln Asp Pro Leu Val Glu Asn Thr Lys Lys 195 200 205		
Leu Leu Arg Phe Asp Phe Leu Asp Pro Phe Phe Leu Ser Ile Thr Val 210 215 220		
Phe Pro Phe Leu Ile Pro Ile Leu Glu Val Leu Asn Ile Cys Val Phe 225 230 235 240		
Pro Arg Glu Val Thr Asn Phe Leu Arg Lys Ala Val Lys Arg Met Lys 245 250 255		
Glu Ser Arg Leu Glu Asp Thr Gln Lys His Arg Val Asp Phe Leu Gln 260 265 270		
Leu Met Ile Asp Ser His Lys Asn Ser Lys Glu Thr Glu Ser His Lys 275 280 285		
Ala Leu Ser Asp Leu Glu Leu Val Ala Gln Ser Ile Ile Phe Ile Phe 290 295 300		
Ala Gly Tyr Glu Thr Thr Ser Ser Val Leu Ser Phe Ile Met Tyr Glu 305 310 315 320		
Leu Ala Thr His Pro Asp Val Gln Gln Lys Leu Gln Glu Glu Ile Asp 325 330 335		
Ala Val Leu Pro Asn Lys Ala Pro Pro Thr Tyr Asp Thr Val Leu Gln 340 345 350		
Met Glu Tyr Leu Asp Met Val Val Asn Glu Thr Leu Arg Leu Phe Pro 355 360 365		
Ile Ala Met Arg Leu Glu Arg Val Cys Lys Lys Asp Val Glu Ile Asn 370 375 380		
Gly Met Phe Ile Pro Lys Gly Trp Val Val Met Ile Pro Ser Tyr Ala 385 390 395 400		
Leu His Arg Asp Pro Lys Tyr Trp Thr Glu Pro Glu Lys Phe Leu Pro 405 410 415		
Glu Arg Phe Ser Lys Lys Asn Lys Asp Asn Ile Asp Pro Tyr Ile Tyr 420 425 430		
Thr Pro Phe Gly Ser Gly Pro Arg Asn Cys Ile Gly Met Arg Phe Ala 435 440 445		



Leu Met Asn Met Lys Leu Ala Leu Ile Arg Val Leu Gln Asn Phe Ser  
 450 455 460

Phe Lys Pro Cys Lys Glu Thr Gln Ile Pro Leu Lys Leu Ser Leu Gly  
 465 470 475 480

Gly Leu Leu Gln Pro Glu Lys Pro Val Val Leu Lys Val Glu Ser Arg  
 485 490 495

Asp Gly Thr Val Ser Gly Ala  
 500

<210> 11  
 <211> 502  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> CYP3A4

<400> 11

Ala Leu Ile Pro Asp Leu Ala Met Glu Thr Trp Leu Leu Leu Ala Val  
 1 5 10 15

Ser Leu Val Leu Leu Tyr Leu Tyr Gly Thr His Ser His Gly Leu Phe  
 20 25 30

Lys Lys Leu Gly Ile Pro Gly Pro Thr Pro Leu Pro Phe Leu Gly Asn  
 35 40 45

Ile Leu Ser Tyr His Lys Gly Phe Cys Met Phe Asp Met Glu Cys His  
 50 55 60

Lys Lys Tyr Gly Lys Val Trp Gly Phe Tyr Asp Gly Gln Gln Pro Val  
 65 70 75 80

Leu Ala Ile Thr Asp Pro Asp Met Ile Lys Thr Val Leu Val Lys Glu  
 85 90 95

Cys Tyr Ser Val Phe Thr Asn Arg Arg Pro Phe Gly Pro Val Gly Phe  
 100 105 110

Met Lys Ser Ala Ile Ser Ile Ala Glu Asp Glu Glu Trp Lys Arg Leu  
 115 120 125

Arg Ser Leu Leu Ser Pro Thr Phe Thr Ser Gly Lys Leu Lys Glu Met  
 130 135 140

Val Pro Ile Ile Ala Gln Tyr Gly Asp Val Leu Val Arg Asn Leu Arg  
 145 150 155 160

Arg Glu Ala Glu Thr Gly Lys Pro Val Thr Leu Lys Asp Val Phe Gly  
 165 170 175

Ala Tyr Ser Met Asp Val Ile Thr Ser Thr Ser Phe Gly Val Asn Ile  
 180 185 190

Asp Ser Leu Asn Asn Pro Gln Asp Pro Phe Val Glu Asn Thr Lys Lys

195	200	205
Leu Leu Arg Phe Asp Phe	Leu Asp Pro Phe Phe	Leu Ser Ile Thr Val
210	215	220
Phe Pro Phe Leu Ile Pro	Ile Leu Glu Val Leu	Asn Ile Cys Val Phe
225	230	235
Pro Arg Glu Val Thr Asn	Phe Leu Arg Lys Ser	Val Lys Arg Met Lys
245	250	255
Glu Ser Arg Leu Glu Asp Thr	Gln Lys His Arg Val	Asp Phe Leu Gln
260	265	270
Leu Met Ile Asp Ser Gln	Asn Ser Lys Glu Thr	Glu Ser His Lys Ala
275	280	285
Leu Ser Asp Leu Glu Leu Val	Ala Gln Ser Ile Ile	Phe Ile Phe Ala
290	295	300
Gly Tyr Glu Thr Thr Ser	Ser Val Leu Ser Phe	Ile Met Tyr Glu Leu
305	310	315
Ala Thr His Pro Val Asp	Gln Gln Lys Leu Gln	Glu Glu Ile Asp Ala
325	330	335
Val Leu Pro Asn Lys Ala	Pro Pro Thr Tyr Asp	Thr Val Leu Gln Met
340	345	350
Glu Tyr Leu Asp Met Val	Val Asn Glu Thr Leu	Arg Leu Phe Pro Ile
355	360	365
Ala Met Arg Leu Glu Arg	Val Cys Lys Lys Asp	Val Glu Ile Asn Gly
370	375	380
Met Phe Ile Pro Lys Gly	Trp Val Val Met Ile	Pro Ser Tyr Ala Leu
385	390	395
His Arg Asp Pro Lys Tyr	Met Thr Glu Pro Glu	Lys Phe Leu Pro Glu
405	410	415
Arg Phe Ser Lys Lys Asn	Lys Asp Asn Ile Asp	Pro Tyr Ile Tyr Thr
420	425	430
Pro Phe Gly Ser Gly Pro	Arg Asn Cys Ile Gly	Met Arg Phe Ala Leu
435	440	445
Met Asn Met Lys Leu Ala	Leu Ile Arg Val Leu	Gln Asn Phe Ser Phe
450	455	460
Lys Pro Cys Lys Glu Thr	Gln Ile Pro Leu Lys	Leu Ser Leu Gly Gly
465	470	475
Leu Leu Gln Pro Glu Lys	Pro Val Val Leu Lys	Val Glu Ser Arg Asp
485	490	495
Gly Thr Val Ser Gly Ala		
500		

&lt;211&gt; 502

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; CYP3A5

&lt;400&gt; 12

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Met Asp Leu Ile Pro Asn Leu Ala Val Glu Thr Trp Leu Leu Leu Ala
 1           5           10           15

Val Ser Leu Val Leu Leu Tyr Leu Tyr Gly Thr Arg Thr His Gly Leu
 20           25           30

Phe Lys Arg Leu Gly Ile Pro Gly Pro Thr Pro Leu Pro Leu Leu Gly
 35           40           45

Asn Val Leu Ser Tyr Arg Gln Gly Leu Trp Lys Phe Asp Thr Glu Cys
 50           55           60

Tyr Lys Lys Tyr Gly Lys Met Trp Gly Thr Tyr Glu Gly Gln Leu Pro
 65           70           75           80

Val Leu Ala Ile Thr Asp Pro Asp Val Ile Arg Thr Val Leu Val Lys
 85           90           95

Glu Cys Tyr Ser Val Phe Thr Asn Arg Arg Ser Leu Gly Pro Val Gly
 100          105          110

Phe Met Lys Ser Ala Ile Ser Leu Ala Glu Asp Glu Glu Trp Lys Arg
 115          120          125

Ile Arg Ser Leu Leu Ser Pro Thr Phe Thr Ser Gly Lys Leu Lys Glu
 130          135          140

Met Phe Pro Ile Ile Ala Gln Tyr Gly Asp Val Leu Val Arg Asn Leu
 145          150          155          160

Arg Arg Glu Ala Glu Lys Gly Lys Pro Val Thr Leu Lys Asp Ile Phe
 165          170          175

Gly Ala Tyr Ser Met Asp Val Ile Thr Gly Thr Ser Phe Gly Val Asn
 180          185          190

Ile Asp Ser Leu Asn Asn Pro Gln Asp Pro Phe Val Glu Ser Thr Lys
 195          200          205

Lys Phe Leu Lys Phe Gly Phe Leu Asp Pro Leu Phe Leu Ser Ile Ile
 210          215          220

Leu Phe Pro Phe Leu Thr Pro Val Phe Glu Ala Leu Asn Val Ser Leu
 225          230          235          240

Phe Pro Lys Asp Thr Ile Asn Phe Leu Ser Lys Ser Val Asn Arg Met
 245          250          255

Lys Lys Ser Arg Leu Asn Asp Lys Gln Lys His Arg Leu Asp Phe Leu
 260          265          270

Gln Leu Met Ile Asp Ser Gln Asn Ser Lys Glu Thr Glu Ser His Lys

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275					280					285					
Ala	Leu	Ser	Asp	Leu	Glu	Leu	Ala	Ala	Gln	Ser	Ile	Ile	Phe	Ile	Phe
290					295					300					
Ala	Gly	Tyr	Glu	Thr	Thr	Ser	Ser	Val	Leu	Ser	Phe	Thr	Leu	Tyr	Glu
305					310					315					
Leu	Ala	Thr	His	Pro	Asp	Val	Gln	Gln	Lys	Leu	Gln	Lys	Glu	Ile	Asp
325					330					335					
Ala	Val	Leu	Pro	Asn	Lys	Ala	Pro	Pro	Thr	Tyr	Asp	Ala	Val	Val	Gln
340					345					350					
Met	Glu	Tyr	Leu	Asp	Met	Val	Val	Asn	Glu	Thr	Leu	Arg	Leu	Phe	Pro
355					360					365					
Val	Ala	Ile	Arg	Leu	Glu	Arg	Thr	Cys	Lys	Lys	Asp	Val	Glu	Ile	Asn
370					375					380					
Gly	Val	Phe	Ile	Pro	Lys	Gly	Ser	Met	Val	Val	Ile	Pro	Thr	Tyr	Ala
385					390					395					
Leu	His	His	Asp	Pro	Lys	Tyr	Trp	Thr	Glu	Pro	Glu	Glu	Phe	Arg	Pro
405					410					415					
Glu	Arg	Phe	Ser	Lys	Lys	Lys	Asp	Ser	Ile	Asp	Pro	Tyr	Ile	Tyr	Thr
420					425					430					
Pro	Phe	Gly	Thr	Gly	Pro	Arg	Asn	Cys	Ile	Gly	Met	Arg	Phe	Ala	Leu
435					440					445					
Met	Asn	Met	Lys	Leu	Ala	Leu	Ile	Arg	Val	Leu	Gln	Asn	Phe	Ser	Phe
450					455					460					
Lys	Pro	Cys	Lys	Glu	Thr	Gln	Ile	Pro	Leu	Lys	Leu	Asp	Thr	Gln	Gly
465					470					475					
Leu	Leu	Gln	Pro	Glu	Lys	Pro	Ile	Val	Leu	Lys	Val	Asp	Ser	Arg	Asp
485					490					495					
Gly	Thr	Leu	Ser	Gly	Glu										
500															

&lt;210&gt; 13

&lt;211&gt; 503

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; CYP3A43

&lt;400&gt; 13

Met	Asp	Leu	Ile	Pro	Asn	Phe	Ala	Met	Glu	Thr	Trp	Val	Leu	Val	Ala
1				5					10					15	

Thr	Ser	Leu	Val	Leu	Leu	Tyr	Ile	Tyr	Gly	Thr	His	Ser	His	Lys	Leu
			20					25					30		

Phe Lys Lys Leu Gly Ile Pro Gly Pro Thr Pro Leu Pro Phe Leu Gly  
 35 40 45  
 Thr Ile Leu Phe Tyr Leu Arg Gly Leu Trp Asn Phe Asp Arg Glu Cys  
 50 55 60  
 Asn Glu Lys Tyr Gly Glu Met Trp Gly Leu Tyr Glu Gly Gln Gln Pro  
 65 70 75 80  
 Met Leu Val Ile Met Asp Pro Asp Met Ile Lys Thr Val Leu Val Lys  
 85 90 95  
 Glu Cys Tyr Ser Val Phe Thr Asn Gln Met Pro Leu Gly Pro Met Gly  
 100 105 110  
 Phe Leu Lys Ser Ala Leu Ser Phe Ala Glu Asp Glu Glu Trp Lys Arg  
 115 120 125  
 Ile Arg Thr Leu Leu Ser Pro Ala Phe Thr Ser Val Lys Phe Lys Glu  
 130 135 140  
 Met Val Pro Ile Ile Ser Gln Cys Gly Asp Met Leu Val Arg Ser Leu  
 145 150 155 160  
 Arg Gln Glu Ala Glu Asn Ser Lys Ser Ile Asn Leu Lys Asp Phe Phe  
 165 170 175  
 Gly Ala Tyr Thr Met Asp Val Ile Thr Gly Thr Leu Phe Gly Val Asn  
 180 185 190  
 Leu Asp Ser Leu Asn Asn Pro Gln Asp Pro Phe Leu Lys Asn Met Lys  
 195 200 205  
 Lys Leu Leu Lys Leu Asp Phe Leu Asp Pro Phe Leu Leu Leu Ile Ser  
 210 215 220  
 Leu Phe Pro Phe Leu Thr Pro Val Phe Glu Ala Leu Asn Ile Gly Leu  
 225 230 235 240  
 Phe Pro Lys Asp Val Thr His Phe Leu Lys Asn Ser Ile Glu Arg Met  
 245 250 255  
 Lys Glu Ser Arg Leu Lys Asp Lys Gln Lys His Arg Val Asp Phe Phe  
 260 265 270  
 Gln Gln Met Ile Asp Ser Gln Asn Ser Lys Glu Thr Lys Ser His Lys  
 275 280 285  
 Ala Leu Ser Asp Leu Glu Leu Val Ala Gln Ser Ile Ile Ile Ile Phe  
 290 295 300  
 Ala Ala Tyr Asp Thr Thr Ser Thr Thr Leu Pro Phe Ile Met Tyr Glu  
 305 310 315 320  
 Leu Ala Thr His Pro Asp Val Gln Gln Lys Leu Gln Glu Glu Ile Asp  
 325 330 335  
 Ala Val Leu Pro Asn Lys Ala Pro Val Thr Tyr Asp Ala Leu Val Gln  
 340 345 350  
 Met Glu Tyr Leu Asp Met Val Val Asn Glu Thr Leu Arg Leu Phe Pro

355                      360                      365  
 Val Val Ser Arg Val Thr Arg Val Cys Lys Lys Asp Ile Glu Ile Asn  
 370                      375                      380  
 Gly Val Phe Ile Pro Lys Gly Leu Ala Val Met Val Pro Ile Tyr Ala  
 385                      390                      395                      400  
 Leu His His Asp Pro Lys Tyr Trp Thr Glu Pro Glu Lys Phe Cys Pro  
 405                      410                      415  
 Glu Arg Phe Ser Lys Lys Asn Lys Asp Ser Ile Asp Leu Tyr Arg Tyr  
 420                      425                      430  
 Ile Pro Phe Gly Ala Gly Pro Arg Asn Cys Ile Gly Met Arg Phe Ala  
 435                      440                      445  
 Leu Thr Asn Ile Lys Leu Ala Val Ile Arg Ala Leu Gln Asn Phe Ser  
 450                      455                      460  
 Phe Lys Pro Cys Lys Glu Thr Gln Ile Pro Leu Lys Leu Asp Asn Leu  
 465                      470                      475                      480  
 Pro Ile Leu Gln Pro Glu Lys Pro Ile Val Leu Lys Val His Leu Arg  
 485                      490                      495  
 Asp Gly Ile Thr Ser Gly Pro  
 500

<210> 14  
 <211> 501  
 <212> PRT  
 <213> Rabbit

<220>  
 <223> CYP3A6

<400> 14

Met Asp Leu Ile Phe Ser Leu Glu Thr Trp Val Leu Leu Ala Ala Ser  
 1                      5                      10                      15  
 Leu Val Leu Leu Tyr Leu Tyr Gly Thr Ser Thr His Gly Leu Phe Lys  
 20                      25                      30  
 Lys Met Gly Ile Pro Gly Pro Thr Pro Leu Pro Phe Ile Gly Thr Ile  
 35                      40                      45  
 Leu Glu Tyr Arg Lys Gly Ile Trp Asp Phe Asp Ile Glu Cys Arg Lys  
 50                      55                      60  
 Lys Tyr Gly Lys Met Trp Gly Leu Phe Asp Gly Arg Gln Pro Leu Met  
 65                      70                      75                      80  
 Val Ile Thr Asp Pro Asp Met Ile Lys Thr Val Leu Val Lys Glu Cys  
 85                      90                      95  
 Tyr Ser Val Phe Thr Asn Arg Arg Ser Phe Gly Pro Val Gly Phe Met  
 100                      105                      110

Lys Lys Ala Val Ser Ile Ser Glu Asp Glu Asp Trp Lys Arg Val Arg  
 115 120 125  
 Thr Leu Leu Ser Pro Thr Phe Thr Ser Gly Lys Leu Lys Glu Met Leu  
 130 135 140  
 Pro Ile Ile Ala Gln Tyr Gly Asp Val Leu Val Lys Asn Leu Arg Gln  
 145 150 155 160  
 Glu Ala Glu Lys Gly Lys Pro Val Asp Leu Lys Glu Ile Phe Gly Ala  
 165 170 175  
 Tyr Ser Met Asp Val Ile Thr Gly Thr Ser Phe Gly Val Asn Ile Asp  
 180 185 190  
 Ser Leu Arg Asn Pro Gln Asp Pro Phe Val Lys Asn Val Arg Arg Leu  
 195 200 205  
 Leu Lys Phe Ser Phe Phe Asp Pro Leu Leu Leu Ser Ile Thr Leu Phe  
 210 215 220  
 Pro Phe Leu Thr Pro Ile Phe Glu Ala Leu His Ile Ser Met Phe Pro  
 225 230 235 240  
 Lys Asp Val Met Asp Phe Leu Lys Thr Ser Val Glu Lys Ile Lys Asp  
 245 250 255  
 Asp Arg Leu Lys Asp Lys Gln Lys Arg Arg Val Asp Phe Leu Gln Leu  
 260 265 270  
 Met Ile Asn Ser Gln Asn Ser Lys Glu Ile Asp Ser His Lys Ala Leu  
 275 280 285  
 Asp Asp Ile Glu Val Val Ala Gln Ser Ile Ile Ile Leu Phe Ala Gly  
 290 295 300  
 Tyr Glu Thr Thr Ser Ser Thr Leu Ser Phe Ile Met His Leu Leu Ala  
 305 310 315 320  
 Thr His Pro Asp Val Gln Gln Lys Leu Gln Glu Glu Ile Asp Thr Leu  
 325 330 335  
 Leu Pro Asn Lys Glu Leu Ala Thr Tyr Asp Thr Leu Val Lys Met Glu  
 340 345 350  
 Tyr Leu Asp Met Val Val Asn Glu Thr Leu Arg Leu Tyr Pro Ile Ala  
 355 360 365  
 Gly Arg Leu Glu Arg Val Cys Lys Lys Asp Val Asp Ile Asn Gly Thr  
 370 375 380  
 Phe Ile Pro Lys Gly Thr Ile Val Met Met Pro Thr Tyr Ala Leu His  
 385 390 395 400  
 Arg Asp Pro Gln His Trp Thr Glu Pro Asp Glu Phe Arg Pro Glu Arg  
 405 410 415  
 Phe Ser Lys Lys Asn Lys Asp Asn Ile Asn Pro Tyr Ile Tyr His Pro  
 420 425 430  
 Phe Gly Ala Gly Pro Arg Asn Cys Leu Gly Met Arg Phe Ala Leu Met

435                      440                      445  
 Asn Ile Lys Leu Ala Leu Val Arg Leu Met Gln Asn Phe Ser Phe Lys  
 450                      455                      460  
 Leu Cys Lys Glu Thr Gln Val Pro Leu Lys Leu Gly Lys Gln Gly Leu  
 465                      470                      475                      480  
 Leu Gln Pro Glu Lys Pro Ile Val Leu Lys Val Val Ser Arg Asp Gly  
 485                      490                      495  
 Ile Ile Arg Gly Ala  
 500

<210> 15  
 <211> 503  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> CYP3A7

<400> 15

Met Asp Leu Ile Pro Asn Leu Ala Val Glu Thr Trp Leu Leu Leu Ala  
 1                      5                      10                      15  
 Val Ser Leu Ile Leu Leu Tyr Leu Tyr Gly Thr Arg Thr His Gly Leu  
 20                      25                      30  
 Phe Lys Lys Leu Gly Ile Pro Gly Pro Thr Pro Leu Pro Phe Leu Gly  
 35                      40                      45  
 Asn Ala Leu Ser Phe Arg Lys Gly Tyr Trp Thr Phe Asp Met Glu Cys  
 50                      55                      60  
 Tyr Lys Lys Tyr Arg Lys Val Trp Gly Ile Tyr Asp Cys Gln Gln Pro  
 65                      70                      75                      80  
 Met Leu Ala Ile Thr Asp Pro Asp Met Ile Lys Thr Val Leu Val Lys  
 85                      90                      95  
 Glu Cys Tyr Ser Val Phe Thr Asn Arg Arg Pro Phe Gly Pro Val Gly  
 100                      105                      110  
 Phe Met Lys Asn Ala Ile Ser Ile Ala Glu Asp Glu Glu Trp Lys Arg  
 115                      120                      125  
 Ile Arg Ser Leu Leu Ser Pro Thr Phe Thr Ser Gly Lys Leu Lys Glu  
 130                      135                      140  
 Met Val Pro Ile Ile Ala Gln Tyr Gly Asp Val Leu Val Arg Asn Leu  
 145                      150                      155                      160  
 Arg Arg Glu Ala Glu Thr Gly Lys Pro Val Thr Leu Lys His Val Phe  
 165                      170                      175  
 Gly Ala Tyr Ser Met Asp Val Ile Thr Ser Thr Ser Phe Gly Val Ser  
 180                      185                      190



Ile Asp Ser Leu Asn Asn Pro Gln Asp Pro Phe Val Glu Asn Thr Lys  
 195 200 205  
 Lys Leu Leu Arg Phe Asn Pro Leu Asp Pro Phe Val Leu Ser Ile Lys  
 210 215 220  
 Val Phe Pro Phe Leu Thr Pro Ile Leu Glu Ala Leu Asn Ile Thr Val  
 225 230 235 240  
 Phe Pro Arg Lys Val Ile Ser Phe Leu Thr Lys Ser Val Lys Gln Ile  
 245 250 255  
 Lys Glu Gly Arg Leu Lys Glu Thr Gln Lys His Arg Val Asp Phe Leu  
 260 265 270  
 Gln Leu Met Ile Asp Ser Gln Asn Ser Lys Asp Ser Glu Thr His Lys  
 275 280 285  
 Ala Leu Ser Asp Leu Glu Leu Met Ala Gln Ser Ile Ile Phe Ile Phe  
 290 295 300  
 Ala Gly Tyr Glu Thr Thr Ser Ser Val Leu Ser Phe Ile Ile Tyr Glu  
 305 310 315 320  
 Leu Ala Thr His Pro Asp Val Gln Gln Lys Val Gln Lys Glu Ile Asp  
 325 330 335  
 Thr Val Leu Pro Asn Lys Ala Pro Pro Thr Tyr Asp Thr Val Leu Gln  
 340 345 350  
 Leu Glu Tyr Leu Asp Met Val Val Asn Glu Thr Leu Arg Leu Phe Pro  
 355 360 365  
 Val Ala Met Arg Leu Glu Arg Val Cys Lys Lys Asp Val Glu Ile Asn  
 370 375 380  
 Gly Met Phe Ile Pro Lys Gly Val Val Val Met Ile Pro Ser Tyr Val  
 385 390 395 400  
 Leu His His Asp Pro Lys Tyr Trp Thr Glu Pro Glu Lys Phe Leu Pro  
 405 410 415  
 Glu Arg Phe Ser Lys Lys Asn Lys Asp Asn Ile Asp Pro Tyr Ile Tyr  
 420 425 430  
 Thr Pro Phe Gly Ser Gly Pro Arg Asn Cys Ile Gly Met Arg Phe Ala  
 435 440 445  
 Leu Val Asn Met Lys Leu Ala Leu Val Arg Val Leu Gln Asn Phe Ser  
 450 455 460  
 Phe Lys Pro Cys Lys Glu Thr Gln Ile Pro Leu Lys Leu Arg Phe Gly  
 465 470 475 480  
 Gly Leu Leu Leu Thr Glu Lys Pro Ile Val Leu Lys Ala Glu Ser Arg  
 485 490 495  
 Asp Glu Thr Val Ser Gly Ala  
 500

<210> 16  
 <211> 503  
 <212> PRT  
 <213> Dog

<220>  
 <223> CYP3A12

<400> 16

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Met Asp Leu Ile Pro Ser Phe Ser Thr Glu Thr Trp Leu Leu Leu Ala
1          5          10          15

Ile Ser Leu Val Leu Leu Tyr Leu Tyr Gly Thr Tyr Thr His Gly Ile
20          25          30

Phe Arg Lys Leu Gly Ile Pro Gly Pro Thr Pro Leu Pro Phe Val Gly
35          40          45

Thr Ala Leu Gly Tyr Arg Asn Gly Phe Tyr Val Phe Asp Met Lys Cys
50          55          60

Phe Ser Lys Tyr Gly Arg Met Trp Gly Phe Tyr Asp Gly Arg Gln Pro
65          70          75          80

Val Leu Ala Ile Thr Asp Pro Asp Met Ile Lys Thr Val Leu Val Lys
85          90          95

Glu Cys Tyr Ser Val Phe Thr Asn Arg Arg Thr Leu Gly Pro Val Gly
100          105          110

Phe Met Lys Ser Ala Ile Ser Leu Ser Glu Asp Glu Glu Trp Lys Arg
115          120          125

Met Arg Thr Leu Leu Ser Pro Thr Phe Thr Thr Gly Lys Leu Lys Glu
130          135          140

Met Phe Pro Ile Ile Gly Gln Tyr Gly Asp Val Leu Val Asn Asn Leu
145          150          155          160

Arg Lys Glu Ala Glu Lys Gly Lys Ala Ile Asn Leu Lys Asp Val Phe
165          170          175

Gly Ala Tyr Ser Met Asp Val Ile Thr Ser Thr Ser Phe Gly Val Asn
180          185          190

Ile Asp Ser Leu Asn His Pro Gln Asp Pro Phe Val Glu Asn Thr Lys
195          200          205

Lys Leu Leu Lys Phe Asp Phe Leu Asp Pro Phe Phe Phe Ser Ile Leu
210          215          220

Leu Phe Pro Phe Leu Thr Pro Val Phe Glu Ile Leu Asn Ile Trp Leu
225          230          235          240

Phe Pro Lys Lys Val Thr Asp Phe Phe Arg Lys Ser Val Glu Arg Met
245          250          255

Lys Glu Ser Arg Leu Lys Asp Lys Gln Lys His Arg Val Asp Phe Leu
260          265          270

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Gln Leu Met Ile Asn Ser Gln Asn Ser Lys Glu Met Asp Thr His Lys  
 275 280 285  
 Ala Leu Ser Asp Leu Glu Leu Val Ala Gln Ser Ile Ile Phe Ile Phe  
 290 295 300  
 Ala Gly Tyr Glu Thr Thr Ser Thr Ser Leu Ser Phe Leu Met Tyr Glu  
 305 310 315 320  
 Leu Ala Thr His Pro Asp Val Gln Gln Lys Leu Gln Glu Glu Ile Asp  
 325 330 335  
 Ala Thr Phe Pro Asn Lys Ala Leu Pro Thr Tyr Asp Ala Leu Val Gln  
 340 345 350  
 Met Glu Tyr Leu Asp Met Val Leu Asn Glu Thr Leu Arg Leu Tyr Pro  
 355 360 365  
 Ile Ala Gly Arg Leu Glu Arg Val Cys Lys Lys Asp Val Glu Ile Ser  
 370 375 380  
 Gly Val Phe Ile Pro Lys Gly Thr Val Val Met Val Pro Thr Phe Thr  
 385 390 395 400  
 Leu His Arg Asp Gln Ser Leu Trp Pro Glu Pro Glu Glu Phe Arg Pro  
 405 410 415  
 Glu Arg Phe Ser Arg Lys Asn Lys Asp Ser Ile Asn Pro Tyr Thr Tyr  
 420 425 430  
 Leu Pro Phe Gly Thr Gly Pro Arg Asn Cys Ile Gly Met Arg Phe Ala  
 435 440 445  
 Ile Met Asn Met Lys Leu Ala Leu Val Arg Val Leu Gln Asn Phe Ser  
 450 455 460  
 Phe Lys Pro Cys Lys Glu Thr Gln Ile Pro Leu Lys Leu Asn Ala Gln  
 465 470 475 480  
 Gly Ile Ile Gln Pro Glu Lys Pro Ile Val Leu Lys Val Glu Pro Arg  
 485 490 495  
 Asp Gly Ser Val Asn Gly Ala  
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&lt;210&gt; 17

&lt;211&gt; 503

&lt;212&gt; PRT

&lt;213&gt; Pig

&lt;220&gt;

&lt;223&gt; CYP3A29

&lt;400&gt; 17

Met Asp Leu Ile Pro Gly Phe Ser Thr Glu Thr Trp Val Leu Leu Ala  
 1 5 10 15

Thr Ser Leu Val Leu Leu Tyr Leu Tyr Gly Thr Tyr Ser His Gly Leu  
 20 25 30

Phe Lys Lys Leu Gly Ile Pro Gly Pro Arg Pro Leu Pro Tyr Phe Gly  
 35 40 45  
 Asn Ile Leu Gly Tyr Arg Lys Gly Val Asp His Phe Asp Lys Lys Cys  
 50 55 60  
 Phe Gln Gln Tyr Gly Lys Met Trp Gly Val Tyr Asp Gly Arg Gln Pro  
 65 70 75 80  
 Leu Leu Ala Val Thr Asp Pro Asn Met Ile Lys Ser Val Leu Val Lys  
 85 90 95  
 Glu Cys Tyr Ser Val Phe Thr Asn Arg Arg Ser Phe Gly Pro Leu Gly  
 100 105 110  
 Ala Met Arg Asn Ala Leu Ser Leu Ala Glu Asp Glu Glu Trp Lys Arg  
 115 120 125  
 Ile Arg Thr Leu Leu Ser Pro Thr Phe Thr Ser Gly Lys Leu Lys Glu  
 130 135 140  
 Met Phe Pro Ile Ile Ser His Tyr Gly Asp Leu Leu Val Ser Asn Leu  
 145 150 155 160  
 Arg Lys Glu Ala Glu Lys Gly Lys Pro Val Thr Met Lys Asp Ile Phe  
 165 170 175  
 Gly Ala Tyr Ser Met Asp Val Ile Thr Ser Thr Ala Phe Gly Val Asn  
 180 185 190  
 Ile Asp Ser Leu Asn Asn Pro Gln Asp Pro Phe Val Glu Asn Ser Lys  
 195 200 205  
 Lys Leu Leu Lys Phe Ser Phe Phe Asp Pro Phe Leu Leu Ser Leu Ile  
 210 215 220  
 Phe Phe Pro Phe Leu Thr Pro Ile Phe Glu Val Leu Asn Ile Thr Leu  
 225 230 235 240  
 Phe Pro Lys Ser Ser Val Asn Phe Phe Thr Lys Ser Val Lys Arg Met  
 245 250 255  
 Lys Glu Ser Arg Leu Thr Asp Gln Gln Lys Arg Arg Val Asp Leu Leu  
 260 265 270  
 Gln Leu Met Ile Asn Ser Gln Asn Ser Lys Glu Met Asp Pro His Lys  
 275 280 285  
 Ser Leu Ser Asn Glu Glu Leu Val Ala Gln Gly Ile Ile Phe Ile Phe  
 290 295 300  
 Ala Gly Tyr Glu Thr Thr Ser Ser Ala Leu Ser Leu Leu Ala Tyr Glu  
 305 310 315 320  
 Leu Ala Thr His Pro Asp Val Gln Gln Lys Leu Gln Glu Glu Ile Glu  
 325 330 335  
 Ala Thr Phe Pro Asn Lys Ala Pro Pro Thr Tyr Asp Ala Leu Ala Gln  
 340 345 350

Met Glu Tyr Leu Asp Met Val Val Asn Glu Thr Leu Arg Leu Tyr Pro  
 355 360 365

Ile Ala Ala Arg Leu Glu Arg Ala Cys Lys Lys Asp Val Glu Ile His  
 370 375 380

Gly Val Phe Val Pro Lys Gly Thr Val Val Val Val Pro Val Phe Val  
 385 390 395 400

Leu His Arg Asp Pro Asp Leu Trp Pro Glu Pro Glu Glu Phe Arg Pro  
 405 410 415

Glu Arg Phe Ser Lys Lys His Lys Asp Thr Ile Asn Pro Tyr Thr Tyr  
 420 425 430

Leu Pro Phe Gly Thr Gly Pro Arg Asn Cys Ile Gly Met Arg Phe Ala  
 435 440 445

Leu Met Asn Met Lys Leu Ala Leu Val Arg Val Leu Gln Asn Phe Ser  
 450 455 460

Phe Lys Pro Cys Lys Glu Thr Gln Ile Pro Leu Lys Leu Thr Thr Gln  
 465 470 475 480

Gly Leu Thr Gln Pro Glu Lys Pro Val Val Leu Lys Ile Leu Pro Arg  
 485 490 495

Asp Gly Thr Val Ser Gly Ala  
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<211> 503

<212> PRT

<213> Mouse

<220>

<223> CYP3A13

<400> 18

Met Asp Leu Ile Pro Asn Phe Ser Met Glu Thr Trp Met Leu Leu Ala  
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Thr Ser Leu Val Leu Leu Tyr Leu Tyr Gly Thr His Ser His Gly Ile  
 20 25 30

Phe Lys Lys Leu Gly Ile Pro Gly Pro Lys Pro Leu Pro Phe Leu Gly  
 35 40 45

Thr Ile Leu Ala Tyr Gln Lys Gly Phe Trp Glu Cys Asp Ile Gln Cys  
 50 55 60

His Lys Lys Tyr Gly Lys Met Trp Gly Leu Tyr Asp Gly Arg Gln Pro  
 65 70 75 80

Val Leu Ala Ile Thr Asp Pro Asp Ile Ile Lys Thr Val Leu Val Lys  
 85 90 95

Glu Cys Tyr Ser Thr Phe Thr Asn Arg Arg Arg Phe Gly Pro Val Gly  
 100 105 110  
 Ile Leu Lys Lys Ala Ile Ser Ile Ser Glu Asn Glu Glu Trp Lys Arg  
 115 120 125  
 Ile Arg Ala Leu Leu Ser Pro Thr Phe Thr Ser Gly Arg Leu Lys Glu  
 130 135 140  
 Met Phe Pro Ile Ile Asn Gln Phe Thr Asp Val Leu Val Arg Asn Met  
 145 150 155 160  
 Arg Gln Gly Leu Gly Glu Gly Lys Pro Thr Ser Met Lys Asp Ile Phe  
 165 170 175  
 Gly Ala Tyr Ser Met Asp Val Ile Thr Ala Thr Ser Phe Gly Val Asn  
 180 185 190  
 Ile Asp Ser Leu Asn Asn Pro Gln Asp Pro Phe Val Glu Lys Ile Lys  
 195 200 205  
 Lys Leu Leu Lys Phe Asp Ile Phe Asp Pro Leu Phe Leu Ser Val Thr  
 210 215 220  
 Leu Phe Pro Phe Leu Thr Pro Val Phe Asp Ala Leu Asn Val Ser Leu  
 225 230 235 240  
 Phe Pro Arg Asp Val Ile Ser Phe Phe Thr Thr Ser Val Glu Arg Met  
 245 250 255  
 Lys Glu Asn Arg Met Lys Glu Lys Glu Lys Gln Arg Val Asp Phe Leu  
 260 265 270  
 Gln Leu Met Ile Asn Ser Gln Asn Tyr Lys Thr Lys Glu Ser His Lys  
 275 280 285  
 Ala Leu Ser Asp Val Glu Ile Val Ala Gln Ser Val Ile Phe Ile Phe  
 290 295 300  
 Ala Gly Tyr Glu Thr Thr Ser Ser Ala Leu Ser Phe Ala Leu Tyr Leu  
 305 310 315 320  
 Leu Ala Ile His Pro Asp Val Gln Lys Lys Leu Gln Asp Glu Ile Asp  
 325 330 335  
 Ala Ala Leu Pro Asn Lys Ala Pro Ala Thr Tyr Asp Thr Leu Leu Gln  
 340 345 350  
 Met Glu Tyr Leu Asp Met Val Val Asn Glu Thr Leu Arg Leu Tyr Pro  
 355 360 365  
 Ile Ala Gly Arg Leu Glu Arg Val Cys Lys Thr Asp Val Glu Ile Asn  
 370 375 380  
 Gly Leu Phe Ile Pro Lys Gly Thr Val Val Met Ile Pro Thr Phe Ala  
 385 390 395 400  
 Leu His Lys Asp Pro Lys Tyr Trp Pro Glu Pro Glu Glu Phe Arg Pro  
 405 410 415

Glu Arg Phe Ser Lys Lys Asn Gln Asp Ser Ile Asn Pro Tyr Met Tyr  
420 425 430

Leu Pro Phe Gly Ser Gly Pro Arg Asn Cys Ile Gly Met Arg Phe Ala  
435 440 445

Leu Ile Asn Met Lys Val Ala Leu Val Arg Val Leu Gln Asn Phe Thr  
450 455 460

Val Gln Pro Cys Lys Glu Thr Glu Ile Pro Leu Lys Leu Ser Lys Gln  
465 470 475 480

Gly Leu Leu Gln Pro Glu Asn Pro Leu Leu Leu Lys Val Val Ser Arg  
485 490 495

Asp Glu Thr Val Ser Asp Glu  
500